

Exhibit IV



Blast 2 Sequences results

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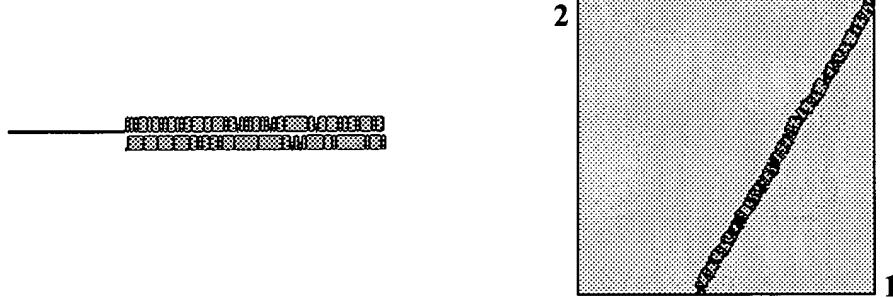
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**x_dropoff: **50** expect: **10.000** wordsize: **3** Filter View option **Standard**Masking character option **X for protein, n for nucleotide** Masking color option **Black** Show CDS translation **Align**

Sequence 1: gi|47117817|sp|O75376|NCOR1_HUMAN Nuclear receptor corepressor 1 (N-CoR1) (N-CoR).
Length = 2440 (1 .. 2440)

SEQ ID NO: 11

Sequence 2: gi|1045655|gb|AAC50236.1|silencing mediator of retinoid and thyroid hormone action
Length = 1495 (1 .. 1495)

HSU37146

NOTE: Bitscore and expect value are calculated based on the size of the nr database.



```

Score = 658 bits (1697), Expect = 0.0
Identities = 556/1576 (35%), Positives = 786/1576 (49%), Gaps = 234/1576 (14%)

Query 993 PCGTS--KSPNREWEVLQPAPH----QVITNLPEGVRLP-----TTRPTRPPPPLIPSSK 1041
      PC TS P EV++ +PH + P G LP T RP P PP I +
Sbjct 25 PCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLPRPTISNPP 84

Query 1042 TTVASEKPSFIMG---GSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQESAK 1098
      ++S K ++ G+ISQG ++ Y++ P VG +++GLP + K
Sbjct 85 PLISSAKHPSVLERQIGAISQG----MSVQLHVYPSEHAKAP-VGPVTMGLPLPMDPKK 138

Query 1099 SATLPYIKQEEFSPRSQNSQPEGLLV-RAQHEGVVRGTA-GAIQEGSITRGTPTSKISVE 1156
      A +KQE+ SPR Q PE L V AQ V+RGTA G++ GSIT+G P++++ +
Sbjct 139 LAPFSGVKQEQLSPRGQAGPPESLGVPATAQEASVLRGTALGSVPGGSITKGIPSTRVPSD 198

Query 1157 SIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSP--EKGREEAASKGHVIYEG 1214
      S + RGSIT GTPA + L KG+I+R+ EDS ++GRE++ KGHVIYEG
  
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Sbjct	199	SAITYRGSITHGTPA-----DVLYKGTTIRIIGEDSPSRLDRGREDSLPGHVIYEG	250
Query	1215	KSGHILSYDNIKNA----REGTRSPRTAHEISL-KRSYESVEGNIKQGMSMRESPVSAP K GH+LSY+ + + G S HE + KR+Y+ +EG + + +S SA	1268
Sbjct	251	KKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAIS-----SAS	304
Query	1269	LEGLICRALP--RGSPHSIDLKERTVLSGSIMQGTPRATTESFEDGLKYP-KQIKRES--- +EGL+ RA+P R SPH LKE+ + GSI QG PR+ E+ ED L+ K +KRE	1322
Sbjct	305	IEGLMGRAIPPERHSPHH-LKEQHHIRGSITQGIPRSYVEAQEDYLRRREAKLLKREGTPP	363
Query	1323	--PPIRAFEGAIT-----KGKP-YDG-ITTIKEMGRSIHEIPRQDILTQESRKTPPEVV PP R A K KP ++G + T+KE GRSIHEIPR+++ R TPE+	1371
Sbjct	364	PPPPSRDLTEAYKTQALGPLKLPAHEGLVATVKEAGRSIHEIPREEL----RHTPELP	418
Query	1372	QSTRPIIEGSISQGTPIKFDDNNSGQSAIK-HNVKSLITGPSKLSRGMPPLIEVPENIKVV + RP+ EGSI+QGTP+K+D + + K H+V+SLI P + + PL+++ + + +	1430
Sbjct	419	LAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDMAD-ARAL	477
Query	1431	ERGKYEDVKAGETVRSRHTSVVSSGPSVLRST---LHEAPKAQLSPGIYDDTSARRTPVS ER YE E+++SR + SSG S+ R + E K + SP Y+D A	1487
Sbjct	478	ERACYE----ESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGA----P	527
Query	1488	YQNTMSRGSPMMNRT----SDVTISSNKSTNHERKSTLTPTQRESIPAKSPVPGVDPVV + + RGSP+ R + ++SS+K++ +RK T TP + AKSP V	1542
Sbjct	528	FAGHLPRGSPVTMREPTPRLQEGSLSSSKASQ-DRKLSTSTPREI---AKSPHSTVPEHH	582
Query	1543	SH--SPFDPHHRGSTAGEVYRSHLPTHLDP-AMPFHRALDPAAAAYLFQRQLSPTPGYPS H SP++ RG + ++YRSH+P DP ++P LD AAAAY R L+P P YP	1599
Sbjct	583	PHPISPYEHLLRGVSGVDLYRSHIPLAFDPTSIPRGIPLD-AAAAYLPRHLAPNPTYPH	641
Query	1600	QYQLY-----AMENTRQTILNDYITSQQMQVN-----RPDVARGLSPREQPLGL Y Y A+EN RQTI+NDYITSQQM N R D+ RGLSPRE L L	1644
Sbjct	642	LYPPYLIRGYPDTAALEN-RQTIINDYITSQQMHHTATAMAQRADMLRGLSPRESSLAL	700
Query	1645	PYPA-TRGIIDLTNMPPT-ILVPHPGGTSTPPMDRITYIPGTQITFPPRPYNSASMSPGH Y A RGIIDL+ +P +LVP GT MDR+ Y+P F R ++S+ +SPG	1702
Sbjct	701	NYAAGPRGIIDLSQLQVPHLPVLVPPPTPGPATAMDRLAYLPTAPQPFSSR-HSSSPSPGG	759
Query	1703	PTHLA---AAASAERERERERERER---IAAASSDL---YLRPGSEQPG----- PTHL +S+ERER+R+RE++R+RER I +++ + RPG+EQ	1746
Sbjct	760	PTHLTKPTTSSSERERDRDRERDREREKSILTSTTVEHAPIWRPGTEQSSGSSGSS	819
Query	1747	-----RPGSHGYVRSPSP-SVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMP RP SH + SP S RTQ+ LQQRPSV T +IT ++P+ +	1797
Sbjct	820	GGGGGSSSRPASHSHAHQHSPISPRTDQDA-LQQRPSVLHNTGMKGIITAVEPSKPTVLR	878
Query	1798	LPAGGPSISQGLPASRYNTAADA-LAALVDAASAPQMDVSKTKESKHEARLEENLRSR P PA+ + A L +D V KE+ A	1856
Sbjct	879	TSTSSPV---RPAATFPATHCPLGGTLGVYPTLMEPVLLPKEARVAR-----	925
Query	1857	SAAVSEQQOLEQKTLVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYE E+ + + + K + ++ PS +P V PP S +	1916
Sbjct	926	----PERPRADTGHAFIAKPPARSGLEPASSPSKGSEPRPLV-----PPVSGHA	970
Query	1917	EELRTRGKTTITAANFIDVIITRQIASDKDARERGSQSSDSS-----SSLSSHRYETPS RT K A + AS D +QS S SL H	1970
Sbjct	971	TIARTPAKNL--APHHASPDPPAPPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSP	1028
Query	1971	DAIEVISPASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGP-----LHHYRP-- + +E +SP SSP+ +K E + + E + + GP L H RP	2019

Sbjct	1029	EGVEPVSPVSSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLP	1088
Query	2020	-QQESPSPQQQLPPSSQAEGMGQVPRTHRLLTADHICQIITQDFARNQVSS-QTPQQPP Q S SP Q P + R++TLA HI ++ITQD+ R+ P P	2077
Sbjct	1089	ESQPSSSPLLQTAPGVKGH-----QRVVTLAQHISEVITQDYTRHHPQQLSAPLPAP	1140
Query	2078	TSTFQNNSPSALVSTPVRTKTSNRYSPESQAQS VHHQRPGSRVSPENLVDKSRGSRPGKSP +F + ++ +R S+ Y P H P +R SP S G + P	2137
Sbjct	1141	LYSFPGASC PVLD--LRRPPSDLYLPPP D----HGAP-ARGSPH----SEGGKRSPEP	1187
Query	2138	ERSHV---SSEPYEPISPPQ--VPVVHEKQDSLLL SQRGAEPAEQRNDARSPGSISYLP ++ V + EP+SPP+ H + LL + G + R ++SPG+ S P	2192
Sbjct	1188	NKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPP	1247
Query	2193	SFFT KL-ENTSPMVKS KKQE IFRKL N SGGD SDMAA QPGTE IFNLP AVTTSGVSSRG +FF+KL E+ S MVKS KKQE I +KLN+ + + +QPGTE IFN+PA+T +G ++ R	2251
Sbjct	1248	AFFSKL TESNSAMVKS KKQE INKKLN THNRNEPEYNISQPGTE IFNMPAITGTGLMTYRS	1307
Query	2252	HSFADPAS-NLGLEDIIRKALMGSFDDKV EDHGV VMS--QPMGVVPGTANTSVVTSGE TR + + AS N+GLE IIRKALMG +D E + + P+ +T+ + R	2308
Sbjct	1308	QAVQEHA STNM GLEAIIRKALMGKYDQWEES PPL SANAFNPLNASASLPAAMPITAADGR	1367
Query	2309	REEGDPSPHSGGVCKPKLISKNSRKS KSPI PGQGYLGTERPSSVSSVHSEG DYHRQTP- + SP GG K K+ + +SRK+KSP P G +RP SVSSVHSEG D +R+TP	2367
Sbjct	1368	SDHTLTSPGGGG--KAKVSGR PSSRKAKSPAP--GLASGDRPPSVSSVHSEG DCN RRTPL	1423
Query	2368	-GWA WEDRPSSTGSTQFPYNPLTM RM--LSSTPPTPIACAPS A VNQA PHQONRIWERE WEDR PSS GST FPYNPL MR+ + ++PP P A S A PH W+ E	2423
Sbjct	1424	TN RVWEDR PSSAGSTPF PYNPLIM RLQAGVMAS PPPPGLPAGSG-PLAGPH---HAWDEE	1479
Query	2424	PAPLLSAQYETLSDSD 2439 P PLL +QYETLSDS+	
Sbjct	1480	PKPLLCSQYETLSDSE 1495	

CPU time: 0.14 user secs. 0.01 sys. secs 0.15 total secs.

Lambda	K	H
0.308	0.126	0.355

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 35,614
 Number of extensions: 21670
 Number of successful extensions: 45
 Number of sequences better than 10.0: 1
 Number of HSP's gapped: 3
 Number of HSP's successfully gapped: 1
 Length of query: 2440
 Length of database: 1,196,146,007
 Length adjustment: 151
 Effective length of query: 2289
 Effective length of database: 1,196,145,856

Effective search space: 2737977864384
Effective search space used: 2737977864384
Neighboring words threshold: 9
X1: 16 (7.1 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.7 bits)
S2: 87 (38.1 bits)